Application No: 10612665   Version No: 2.0

Input Set:

Output Set:

Started:	2008-07-03 12:49:22.058
Finished:	2008-07-03 12:49:26.101
Elapsed:	0 hr(s) 0 min(s) 4 sec(s) 43 ms
Total Warnings:	205
Total Errors:	0
No. of SeqIDs Defined:	211
Actual SeqID Count:	211

Error code   Error Description

W   213   Artificial or Unknown found in <213> in SEQ ID (5)

W   213   Artificial or Unknown found in <213> in SEQ ID (8)

W   213   Artificial or Unknown found in <213> in SEQ ID (9)

W   213   Artificial or Unknown found in <213> in SEQ ID (10)

W   213   Artificial or Unknown found in <213> in SEQ ID (11)

W   213   Artificial or Unknown found in <213> in SEQ ID (12)

W   213   Artificial or Unknown found in <213> in SEQ ID (13)

W   213   Artificial or Unknown found in <213> in SEQ ID (14)

W   213   Artificial or Unknown found in <213> in SEQ ID (15)

W   213   Artificial or Unknown found in <213> in SEQ ID (16)

W   213   Artificial or Unknown found in <213> in SEQ ID (17)

W   213   Artificial or Unknown found in <213> in SEQ ID (18)

W   213   Artificial or Unknown found in <213> in SEQ ID (19)

W   213   Artificial or Unknown found in <213> in SEQ ID (20)

W   213   Artificial or Unknown found in <213> in SEQ ID (21)

W   213   Artificial or Unknown found in <213> in SEQ ID (22)

W   213   Artificial or Unknown found in <213> in SEQ ID (23)

W   213   Artificial or Unknown found in <213> in SEQ ID (24)

W   213   Artificial or Unknown found in <213> in SEQ ID (25)

W   213   Artificial or Unknown found in <213> in SEQ ID (26)

Input Set:

Output Set:

Started:	2008-07-03 12:49:22.058
Finished:	2008-07-03 12:49:26.101
Elapsed:	0 hr(s) 0 min(s) 4 sec(s) 43 ms
Total Warnings:	205
Total Errors:	0
No. of SeqIDs Defined:	211
Actual SeqID Count:	211

Error code   Error Description

This error has occured more than 20 times, will not be displayed

<210> 1
<211> 5
<212> PRT
<213> Homo sapiens

<400> 1

Val Leu Gln Arg Tyr
1   5

<210> 2
<211> 8
<212> PRT
<213> Homo sapiens

<400> 2

Thr Lys Val Asn Phe Tyr Ala Trp
1   5

<210> 3
<211> 9
<212> PRT
<213> Homo sapiens

<400> 3

Ser Gly Leu Arg Ser Leu Thr Thr Leu
1   5

<210> 4
<211> 6
<212> PRT
<213> Homo sapiens

<400> 4

Ser Asn Phe Leu Arg Gly
1   5

<210> 5
<211> 6059
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: plasmid

<400> 5
ctagagtcga cccgggcggc cgcttccctt tagtgagggt taatgcttcg agcagacatg   60

ataagataca ttgatgagtt tggacaaacc acaactagaa tgcagtgaaa aaaatgcttt   120

atttgtgaaa tttgtgatgc tattgcttta tttgtaacca ttataagctg caataaacaa   180

gttaacaaca acaattgcat tcattttatg tttcaggttc aggggggagat gtgggaggtt   240

ttttaaagca agtaaaacct ctacaaatgt ggtaaaatcc dataaggatc gatccgggct   300

ggcgtaatag cgaagaggcc cgcaccgatc gcccttccca acagttgcgc agcctgaatg   360

gcgaatggac gcgccctgta gcggcgcatt aagcgcggcg ggtgtggtgg ttacgcgcag   420

cgtgaccgct acacttgcca gcgccctagc gcccgctcct ttcgctttct cccttcctt   480

tctcgccacg ttcgccggct ttccccgtca agctctaaat cggggggctcc ctttagggtt   540

ccgatttagt gctttacggc acctcgaccc caaaaaactt gattagggtg atggttcacg   600

tagtgggcca tcgccctgat agacggtttt tcgcccttg acgttggagt ccacgttctt   660

taatagtgga ctcttgttcc aaactggaac aacactcaac cctatctcgg tctattctt   720

tgatttataa gggattttgc cgatttcggc ctattggtta aaaaatgagc tgatttaaca   780

```
aaaatttaac gcgaatttta acaaaatatt aacgcttaca atttcctgat gcggtatttt    840

ctccttacgc atctgtgcgg tatttcacac cgcatacgcg gatctgcgca gcaccatggc    900

ctgaaataac ctctgaaaga ggaacttggt taggtacctt ctgaggcgga aagaaccagc    960

tgtggaatgt gtgtcagtta gggtgtggaa agtccccagg ctccccagca ggcagaagta   1020

tgcaaagcat gcatctcaat tagtcagcaa ccaggtgtgg aaagtcccca ggctccccag   1080

caggcagaag tatgcaaagc atgcatctca attagtcagc aaccatagtc ccgcccctaa   1140

ctccgcccat cccgcccta actccgccca gttccgccca ttctccgccc catggctgac   1200

taattttttt tatttatgca gaggccgagg ccgcctcggc ctctgagcta ttccagaagt   1260

agtgaggagg cttttttgga ggcctaggct tttgcaaaaa gcttgattct tctgacacaa   1320

cagtctcgaa cttaaggcta gagccaccat gattgaacaa gatggattgc acgcaggttc   1380

tccggccgct tgggtggaga ggctattcgg ctatgactgg gcacaacaga caatcggctg   1440

ctctgatgcc gccgtgttcc ggctgtcagc gcaggggcgc ccggttcttt ttgtcaagac   1500

cgacctgtcc ggtgccctga atgaactgca ggacgaggca gcgcggctat cgtggctggc   1560

cacgacgggc gttccttgcg cagctgtgct cgacgttgtc actgaagcgg gaagggactg   1620

gctgctattg ggcgaagtgc cggggcagga tctcctgtca tctcaccttg ctcctgccga   1680

gaaagtatcc atcatggctg atgcaatgcg gcggctgcat acgcttgatc cggctacctg   1740

cccattcgac caccaagcga aacatcgcat cgagcgagca cgtactcgga tggaagccgg   1800

tcttgtcgat caggatgatc tggacgaaga gcatcagggg ctcgcgccag ccgaactgtt   1860

cgccaggctc aaggcgcgca tgcccgacgg cgaggatctc gtcgtgaccc atggcgatgc   1920

ctgcttgccg aatatcatgg tggaaaatgg ccgcttttct ggattcatcg actgtggccg   1980

gctgggtgtg gcggaccgct atcaggacat agcgttggct acccgtgata ttgctgaaga   2040

gcttggcggc gaatgggctg accgcttcct cgtgctttac ggtatcgccg ctcccgattc   2100

gcagcgcatc gccttctatc gccttcttga cgagttcttc tgagcgggac tctggggttc   2160

gaaatgaccg accaagcgac gcccaacctg ccatcacgat ggccgcaata aaatatcttt   2220

attttcatta catctgtgtg ttggtttttt gtgtgaatcg atagcgataa ggatccgcgt   2280

atggtgcact ctcagtacaa tctgctctga tgccgcatag ttaagccagc cccgacaccc   2340

gccaacaccc gctgacgcgc cctgacgggc ttgtctgctc ccggcatccg cttacagaca   2400

agctgtgacc gtctccggga gctgcatgtg tcagaggttt tcaccgtcat caccgaaacg   2460
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cgcgagacga aagggcctcg tgatacgcct attttttatag gttaatgtca tgataataat      2520

ggtttcttag acgtcaggtg gcactttcg gggaaatgtg cgcggaaccc ctatttgttt      2580

attttttctaa atacattcaa atatgtatcc gctcatgaga caataaccct gataaatgct      2640

tcaataatat tgaaaaagga agagtatgag tattcaacat ttccgtgtcg cccttattcc      2700

ctttttttgcg gcattttgcc ttcctgtttt tgctcaccca gaaacgctgg tgaaagtaaa      2760

agatgctgaa gatcagttgg gtgcacgagt gggttacatc gaactggatc tcaacagcgg      2820

taagatcctt gagagttttc gccccgaaga acgttttcca atgatgagca cttttaaagt      2880

tctgctatgt ggcgcggtat tatcccgtat tgacgccggg caagagcaac tcggtcgccg      2940

catacactat tctcagaatg acttggttga gtactcacca gtcacagaaa agcatcttac      3000

ggatggcatg acagtaagag aattatgcag tgctgccata accatgagtg ataacactgc      3060

ggccaactta cttctgacaa cgatcggagg accgaaggag ctaaccgctt ttttgcacaa      3120

catggggggat catgtaactc gccttgatcg ttgggaaccg gagctgaatg aagccatacc      3180

aaacgacgag cgtgacacca cgatgcctgt agcaatggca caacgttgc gcaaactatt      3240

aactggcgaa ctacttactc tagcttcccg gcaacaatta atagactgga tggaggcgga      3300

taaagttgca ggaccacttc tgcgctcggc ccttccggct ggctggttta ttgctgataa      3360

atctggagcc ggtgagcgtg ggtctcgcgg tatcattgca gcactggggc cagatggtaa      3420

gccctcccgt atcgtagtta tctacacgac ggggagtcag gcaactatgg atgaacgaaa      3480

tagacagatc gctgagatag gtgcctcact gattaagcat tggtaactgt cagaccaagt      3540

ttactcatat atactttaga ttgatttaaa acttcatttt taatttaaaa ggatctaggt      3600

gaagatcctt tttgataatc tcatgaccaa aatcccttaa cgtgagtttt cgttccactg      3660

agcgtcagac cccgtagaaa agatcaaagg atcttcttga tccttttttt ttctgcgcgt      3720

aatctgctgc ttgcaaacaa aaaaaccacc gctaccagcg gtggtttgtt tgccggatca      3780

agagctacca actctttttc cgaaggtaac tggcttcagc agagcgcaga taccaaatac      3840

tgttcttcta gtgtagccgt agttaggcca ccacttcaag aactctgtag caccgcctac      3900

atacctcgct ctgctaatcc tgttaccagt ggctgctgcc agtggcgata agtcgtgtct      3960

taccgggttg gactcaagac gatagttacc ggataaggcg cagcggtcgg gctgaacggg      4020

gggttcgtgc acacagccca gcttggagcg aacgacctac accgaactga gatacctaca      4080

gcgtgagcta tgagaaagcg ccacgcttcc cgaagggaga aaggcggaca ggtatccggt      4140

aagcggcagg gtcggaacag gagagcgcac gagggagctt ccagggggaa acgcctggta      4200
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tctttatagt cctgtcgggt ttcgccacct ctgacttgag cgtcgatttt tgtgatgctc      4260

gtcagggggg cggagcctat ggaaaaacgc cagcaacgcg gccttttac ggttcctggc       4320

cttttgctgg ccttttgctc acatggctcg acagatcttc aatattggcc attagccata      4380

ttattcattg gttatatagc ataaatcaat attggctatt ggccattgca tacgttgtat      4440

ctatatcata atatgtacat ttatattggc tcatgtccaa tatgaccgcc atgttggcat      4500

tgattattga ctagttatta atagtaatca attacggggt cattagttca tagcccatat      4560

atggagttcc gcgttacata acttacggta aatggcccgc ctggctgacc gcccaacgac      4620

ccccgcccat tgacgtcaat aatgacgtat gttcccatag taacgccaat agggactttc      4680

cattgacgtc aatgggtgga gtatttacgg taaactgccc acttggcagt acatcaagtg      4740

tatcatatgc caagtccgcc ccctattgac gtcaatgacg gtaaatggcc cgcctggcat      4800

tatgcccagt acatgacctt acgggacttt cctacttggc agtacatcta cgtattagtc      4860

atcgctatta ccatggtgat gcggttttgg cagtacacca atgggcgtgg atagcggttt      4920

gactcacggg gatttccaag tctccacccc attgacgtca atgggagttt gttttggcac      4980

caaaatcaac gggactttcc aaaatgtcgt aacaactgcg atcgcccgcc ccgttgacgc      5040

aaatgggcgg taggcgtgta cggtgggagg tctatataag cagagctcgt ttagtgaacc      5100

gtcagatcac tagaagcttt attgcggtag tttatcacag ttaaattgct aacgcagtca      5160

gtgcttctga cacaacagtc tcgaacttaa gctgcagtga ctctcttaag gtagccttgc      5220

agaagttggt cgtgaggcac tgggcaggta agtatcaagg ttacaagaca ggtttaagga      5280

gaccaataga aactgggctt gtcgagacag agaagactct tgcgtttctg ataggcacct      5340

attggtctta ctgacatcca ctttgccttt ctctccacag gtgtccactc ccagttcaat      5400

tacagctctt aaggctagag tacttaatac gactcactat aggctagcct cgagcgcgga      5460

gatgggggtg cacgaatgtc ctgcctggct gtggcttctc ctgtccctgc tgtcgctccc      5520

tctgggcctc ccagtcctgg gcgccccacc acgcctcatc tgtgacagcc gagtcctgga      5580

gaggtacctc ttggaggcca aggaggccga gaatatcacg acgggctgtg ctgaacactg      5640

cagcttgaat gagaatatca ctgtcccaga caccgacgtt aatttctatg cctggaagag      5700

gatggaggtc gggcagcagg ccgtagaagt ctggcagggc ctggccctgc tgtcggaagc      5760

tgtcctgcgg ggccaggccc tgttggtcaa ctcttcccag ccgtgggagc ccctgcagct      5820

gcatgtggat aaagccgtcg agggccttcg cagcctcacc actctgcttc gggctctgcg      5880
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agcccagaag gaagccatct cccctccaga tgcggcctca gctgctccac tccgaacaat   5940

cactgctgac actttccgca aactcttccg agtctactcc aatttcctcc ggggaaagct   6000

gaagctgtac acaggggagg cctgcaggac aggggaccat catcaccatc accattgat   6059

<210> 6
<211> 193
<212> PRT
<213> Homo sapiens

<400> 6

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Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
1               5                   10                  15
Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
            20                  25                  30
Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
        35                  40                  45
Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
    50                  55                  60
Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
65                  70                  75                  80
Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
                85                  90                  95
Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
            100                 105                 110
Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
        115                 120                 125
Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
    130                 135                 140
Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
145                 150                 155                 160
Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
                165                 170                 175
Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
            180                 185                 190
Arg
```


<210> 7
<211> 580
<212> DNA
<213> Homo sapiens

<400> 7
atggggggtgc acgaatgtcc tgcctggctg tggcttctcc tgtccctgct gtcgctccct   60

ctgggcctcc cagtcctggg cgcccccacca cgcctcatct gtgacagccg agtcctggag   120

aggtacctct tggaggccaa ggaggccgag aatatcacga cgggctgtgc tgaacactgc   180

agcttgaatg agaatatcac tgtcccagac accaaagtta atttctatgc ctggaagagg   240

atggaggtcg ggcagcaggc cgtagaagtc tggcagggcc tggccctgct gtcggaagct   300

gtcctgcggg gccaggccct gttggtcaac tcttcccagc cgtgggagcc cctgcactgc   360

atgtggataa agccgtcagt ggccttcgca gcctcaccac tctgcttcgg gctctgggag   420

cccagaagga agccatctcc cctccagatg cggcctcagc tgctccactc cgaacaatca   480

ctgctgacac tttcgcaaac tcttccgagt ctactccaat ttcctccggg gaaagctgaa   540

gctgtacaca ggggaggcct gcaggacagg ggacagatga   580

<210>   8
<211>   35
<212>   DNA
<213>   Artificial

<220>
<223>   Description of Artificial Sequence: primer

<400>   8
agctctcgag gcgcggagat gggggtgcac gaatg   35

<210>   9
<211>   36
<212>   DNA
<213>   Artificial

<220>
<223>   Description of Artificial Sequence: primer

<400>   9
atgctctaga cacacctggt catctgtccc ctgtcc   36

<210> 10
<211> 166
<212> PRT
<213> Artificial Sequence

<220>
<223> mutein

<400> 10
Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu
 1   5   10   15
Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
            20   25   30
Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
        35   40   45
Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
    50   55   60
Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
65   70   75   80
Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
                85   90   95

```
Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
            100                 105                 110
Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
        115                 120                 125
Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
    130                 135                 140
Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
145                 150                 155                 160
Cys Arg Thr Gly Asp Arg
                165
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<210> 11
<211> 45
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: primer

<400> 11
catgtggata aagccgtcga gggccttcgc agcctcacca ctctg   45

<210> 12
<211> 45
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: primer

<400> 12
cagagtggtg aggctgcgaa ggccctcgac ggctttatcc acatg   45

<210> 13
<211> 45
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: primer

<400> 13
gagaatatca ctgtcccaga caccgacgtt aatttctatg cctgg   45

<210> 14
<211> 45
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: primer

<400> 14

<210> 15
<211> 166
<212> PRT
<213> Artificial Sequence

<220>
<223> mutein

<400> 15
Ala Pro Pro Arg Leu Ala Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu
 1   5   10   15
Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
            20   25   30
Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
        35   40   45
Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
    50   55   60
Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
65   70   75   80
Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
                85   90   95
Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
            100   105   110
Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
        115   120   125
Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
    130   135   140
Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
145   150   155   160
Cys Arg Thr Gly Asp Arg
                165

<210> 16
<211> 166
<212> PRT
<213> Artificial Sequence

<220>
<223> mutein

<400> 16
Ala Pro Pro Arg Leu Ile Ala Asp Ser Arg Val Leu Glu Arg Tyr Leu
 1   5   10   15
Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
            20   25   30
Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
        35   40   45
Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
    50   55   60
Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
65   70   75   80
Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
                85   90   95

Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
            100   105   110
Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
            115   120   125
Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
        130   135   140
Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
145   150   155   160
Cys Arg Thr Gly Asp Arg
                165

<210> 17
<211> 166
<212> PRT
<213> Artificial Sequence

<220>
<223> mutein

<400> 17
Ala Pro Pro Arg Leu Ile Cys Asp Ser Ile Val Leu Glu Arg Tyr Leu
 1   5   10   15
Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
            20   25   30
Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
        35   40   45
Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
    50   55   60
Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
65   70   75   80
Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
                85   90   95
Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
            100   105